

MAR 25 2002

LeA34821\_SeqList

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Acetylcholine receptor subunits

<130> Le A 34 821

<140> US/09/941,179

<141> 2001-08-27

<150> DE 100 42 177.6

<151> 2000-08-28

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 45

<212> PRT

<213> Torpedo californica

<400> 1

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Ile Val Thr His Phe Pro Phe Asp Gln Gln Asn Cys Thr  
35 40 45

<210> 2

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1866)

<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 2

atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc 48  
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag 96  
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
20 25 30

gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt 144  
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
35 40 45

ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc 192  
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
50 55 60

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aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp 85 90 95	288
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu 100 105 110	336
atc tgg cgg ccg gac ata gtc ctc tac aac aat gcc gac ggc aac ttc Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe 115 120 125	384
gag gta acg ctg gcg acg aag gcg act ttg aat tat acg gga cgt gtg Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val 130 135 140	432
gag tgg cgc ccg ccg gct atc tac aag tcc tcg tgc gag atc gac gtg Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val 145 150 155 160	480
gaa tac ttc ccg ttc gac cag cag acg tgc gtc atg aag ttc ggc tcg Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser 165 170 175	528
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His 180 185 190	576
gtg gac caa ctg gac tac tgg gaa agc ggg gag tgg gtc atc att aat Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn 195 200 205	624
gcc gtg ggc aat tac aac agc aag aaa tat gaa tgc tgc aca gag atc Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile 210 215 220	672
tac cct gat ata act tac tcc ttc att atc cgg agg ctg ccg ctg ttc Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe 225 230 235 240	720
tac aca atc aat ttg atc att ccc tgc ctg ctt atc tcc tgc ttg act Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr 245 250 255	768
gtc ctg gtc ttc tac cta ccc tct gag tgc gga gag aag ata acc ttg Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu 260 265 270	816
tgc atc tct gtg ctg cta tcc ctc acg gtg ttc ctg ctg ctc atc aca Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr 275 280 285	864
gag atc atc cct tct acc tcc ctg gtc atc ccc ctg ata gga gag tat Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr 290 295 300	912
ctg ctc ttc acc atg ata ttt gtc acc ttg tct atc atc atc act gtc Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val 305 310 315 320	960

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Met	Glu	Pro	Asn	Phe	Thr	Thr	Ser	Ser	Ser	Pro	Ser	Pro	Gln	Ser	Asn	
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Glu	Pro	Ser	Pro	Thr	Ser	Ser	Phe	Cys	Ala	His	Leu	Glu	Glu	Pro	Ala	
				405					410					415		
aaa	cct	atg	tgc	aaa	tcc	cct	tct	gga	cag	tac	tca	atg	ctg	cac	cct	1296
Lys	Pro	Met	Cys	Lys	Ser	Pro	Ser	Gly	Gln	Tyr	Ser	Met	Leu	His	Pro	
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gag	ccc	cca	cag	gtg	acg	tgt	tcc	tct	ccg	aag	ccc	tcc	tgc	cac	ccc	1344
Glu	Pro	Pro	Gln	Val	Thr	Cys	Ser	Ser	Pro	Lys	Pro	Ser	Cys	His	Pro	
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ctg	agt	gac	acc	cag	acc	aca	tct	atc	tca	aaa	ggc	aga	tcg	ctc	agt	1392
Leu	Ser	Asp	Thr	Gln	Thr	Thr	Ser	Ile	Ser	Lys	Gly	Arg	Ser	Leu	Ser	
	450					455					460					
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Val	Gln	Gln	Met	Tyr	Ser	Pro	Asn	Lys	Thr	Glu	Glu	Gly	Ser	Ile	Arg	
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Cys	Arg	Ser	Arg	Ser	Ile	Gln	Tyr	Cys	Tyr	Leu	Gln	Glu	Asp	Ser	Ser	
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cag	acc	aat	ggc	cac	tct	agt	gcc	tct	cca	gcg	tcg	cag	cgc	tgc	cac	1536
Gln	Thr	Asn	Gly	His	Ser	Ser	Ala	Ser	Pro	Ala	Ser	Gln	Arg	Cys	His	
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ctc	aat	gaa	gag	cag	ccc	cag	cac	aag	ccc	cac	cag	tgc	aag	tgt	aag	1584
Leu	Asn	Glu	Glu	Gln	Pro	Gln	His	Lys	Pro	His	Gln	Cys	Lys	Cys	Lys	
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Cys	Arg	Lys	Gly	Glu	Ala	Ala	Gly	Thr	Pro	Thr	Gln	Gly	Ser	Lys	Ser	
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cac	agc	aac	aaa	gga	gaa	cac	ctc	gtg	ctg	atg	tcc	cca	gcc	ctg	aag	1680
His	Ser	Asn	Lys	Gly	Glu	His	Leu	Val	Leu	Met	Ser	Pro	Ala	Leu	Lys	
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ctg	gcg	gtg	gaa	ggg	gtc	cac	tac	att	gca	gac	cac	ctg	cga	gca	gaa	1728
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575

gat gca gat ttc tca gtg aag gaa gac tgg aag tac gta gca atg gtc 1776  
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 Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly  
 595 600 605

acc gtt ggg ctc ttc ctc ccg ccg tgg ctg gca gga atg atc taa 1869  
 Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile  
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&lt;210&gt; 3

&lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

&lt;400&gt; 3

Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
 1 5 10 15

Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30

Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
 35 40 45

Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
 50 55 60

Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80

Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95

Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
 100 105 110

Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe  
 115 120 125

Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val  
 130 135 140

Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val  
 145 150 155 160

Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser  
 165 170 175

Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
 180 185 190

Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn

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195 200 205

Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile  
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Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe  
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Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr  
245 250 255

Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu  
260 265 270

Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr  
275 280 285

Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr  
290 295 300

Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val  
305 310 315 320

Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro  
325 330 335

Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe  
340 345 350

Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu  
355 360 365

Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp  
370 375 380

Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn  
385 390 395 400

Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala  
405 410 415

Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro  
420 425 430

Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro  
435 440 445

Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser  
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Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg  
465 470 475 480

Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser  
485 490 495

Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His  
500 505 510

Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys  
515 520 525

Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser

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530 535 540  
 His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys  
 545 550 555 560  
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 565 570 575  
 Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val  
 580 585 590  
 Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly  
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 Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

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<210> 6  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(1893)  
 <223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

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 Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
 1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag 96  
 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30

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aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp 85 90 95	288
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu 100 105 110	336
atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe 115 120 125	384
gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile 130 135 140	432
aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val 145 150 155 160	480
acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser 165 170 175	528
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His 180 185 190	576
cgc ggg acc aac gtg gtg gag ctg ggc gtg gac caa ctg gac tac tgg Arg Gly Thr Asn Val Val Glu Leu Gly Val Asp Gln Leu Asp Tyr Trp 195 200 205	624
gaa agc ggg gag tgg gtc atc att aat gcc gtg ggc aat tac aac agc Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser 210 215 220	672
aag aaa tat gaa tgc tgc aca gag atc tac cct gat ata act tac tcc Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser 225 230 235 240	720
ttc att atc cgg agg ctg ccg ctg ttc tac aca atc aat ttg atc att Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile 245 250 255	768
ccc tgc ctg ctt atc tcc tgc ttg act gtc ctg gtc ttc tac cta ccc Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro 260 265 270	816
tct gag tgc gga gag aag ata acc ttg tgc atc tct gtg ctg cta tcc Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser 280 285 290 295	864

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ctg gtc atc ccc ctg ata gga gag tat ctg ctc ttc acc atg ata ttt Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe 305 310 315 320			960
gtc acc ttg tct atc atc atc act gtc ttt gtg ctc aac gta cac cac Val Thr Leu Ser Ile Ile Ile Thr Val Phe Val Leu Asn Val His His 325 330 335			1008
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tcc tct ccg aag ccc tcc tgc cac ccc ctg agt gac acc cag acc aca Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr 450 455 460			1392
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 Leu Val Leu Met Ser Pro Ala Leu Lys Leu Ala Val Glu Gly Val His  
 565 570 575  
 tac att gca gac cac ctg cga gca gaa gat gca gat ttc tca gtg aag 1776  
 Tyr Ile Ala Asp His Leu Arg Ala Glu Asp Ala Asp Phe Ser Val Lys  
 580 585 590  
 gaa gac tgg aag tac gta gca atg gtc att gac cgg atc ttt ctc tgg 1824  
 Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp  
 595 600 605  
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 Met Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro  
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 Pro Trp Leu Ala Gly Met Ile  
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<210> 7

<211> 631

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

<400> 7

Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Leu Cys Ala  
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 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30  
 Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
 35 40 45  
 Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
 50 55 60  
 Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80  
 Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95  
 Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
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 Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe  
 115 120 125

LeA34821\_SeqList

Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile  
130 135 140

Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val  
145 150 155 160

Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser  
165 170 175

Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
180 185 190

Arg Gly Thr Asn Val Val Glu Leu Gly Val Asp Gln Leu Asp Tyr Trp  
195 200 205

Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser  
210 215 220

Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser  
225 230 235 240

Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile  
245 250 255

Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro  
260 265 270

Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser  
275 280 285

Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser  
290 295 300

Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe  
305 310 315 320

Val Thr Leu Ser Ile Ile Ile Thr Val Phe Val Leu Asn Val His His  
325 330 335

Arg Ser Pro Arg Thr His Thr Met Pro Asp Trp Val Arg Arg Val Phe  
340 345 350

Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Thr Val  
355 360 365

Lys Asp Asn Cys Lys Lys Leu Ile Glu Ser Met His Lys Leu Thr Asn  
370 375 380

Ser Pro Arg Leu Trp Ser Glu Thr Asp Met Glu Pro Asn Phe Thr Thr  
385 390 395 400

Ser Ser Ser Pro Ser Pro Gln Ser Asn Glu Pro Ser Pro Thr Ser Ser  
405 410 415

Phe Cys Ala His Leu Glu Glu Pro Ala Lys Pro Met Cys Lys Ser Pro  
420 425 430

Ser Gly Gln Tyr Ser Met Leu His Pro Glu Pro Pro Gln Val Thr Cys  
435 440 445

Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr  
450 455 460

LeA34821\_SeqList

Ser Ile Ser Lys Gly Arg Ser Leu Ser Val Gln Gln Met Tyr Ser Pro  
 465 470 475 480  
 Asn Lys Thr Glu Glu Gly Ser Ile Arg Cys Arg Ser Arg Ser Ile Gln  
 485 490 495  
 Tyr Cys Tyr Leu Gln Glu Asp Ser Ser Gln Thr Asn Gly His Ser Ser  
 500 505 510  
 Ala Ser Pro Ala Ser Gln Arg Cys His Leu Asn Glu Glu Gln Pro Gln  
 515 520 525  
 His Lys Pro His Gln Cys Lys Cys Lys Cys Arg Lys Gly Glu Ala Ala  
 530 535 540  
 Gly Thr Pro Thr Gln Gly Ser Lys Ser His Ser Asn Lys Gly Glu His  
 545 550 555 560  
 Leu Val Leu Met Ser Pro Ala Leu Lys Leu Ala Val Glu Gly Val His  
 565 570 575  
 Tyr Ile Ala Asp His Leu Arg Ala Glu Asp Ala Asp Phe Ser Val Lys  
 580 585 590  
 Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp  
 595 600 605  
 Met Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro  
 610 615 620  
 Pro Trp Leu Ala Gly Met Ile  
 625 630

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 gtggaccaac tggactactg g 81

<210> 9  
 <211> 81  
 <212> DNA  
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

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 gtgtctcaag tctatcttag c 81

<210> 10  
 <211> 1869

LeA34821\_SeqList

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1866)

<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

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Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala
1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag 96
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu
20 25 30

gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt 144
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg
35 40 45

ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc 192
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser
50 55 60

ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca 240
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr
65 70 75 80

aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac 288
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp
85 90 95

ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc 336
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu
100 105 110

atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt 384
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe
115 120 125

gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att 432
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile
130 135 140

aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt 480
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val
145 150 155 160

acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct 528
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser
165 170 175

tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat 576
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His
180 185 190

gtc gac ctg tcc gag ttc tac acc tcc gtg gag tgg gac atc ctg gag 624
Val Asp Leu Ser Glu Phe Tyr Thr Ser Val Glu Trp Asp Ile Leu Glu
195 200 205

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## LeA34821\_SeqList

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tac ctg gac ata acg ttt aac ttc att atc cgg agg ctg ccg ctg ttc Tyr Leu Asp Ile Thr Phe Asn Phe Ile Ile Arg Arg Leu Pro Leu Phe 225 230 235 240	720
tac aca atc aat ttg atc att ccc tgc ctg ctt atc tcc tgc ttg act Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr 245 250 255	768
gtc ctg gtc ttc tac cta ccc tct gag tgc gga gag aag ata acc ttg Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu 260 265 270	816
tgc atc tct gtg ctg cta tcc ctc acg gtg ttc ctg ctg ctc atc aca Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr 275 280 285	864
gag atc atc cct tct acc tcc ctg gtc atc ccc ctg ata gga gag tat Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr 290 295 300	912
ctg ctc ttc acc atg ata ttt gtc acc ttg tct atc atc atc act gtc Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val 305 310 315 320	960
ttt gtg ctc aac gta cac cac cgt tca cca cgt acc cac acg atg cct Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro 325 330 335	1008
gac tgg gtg agg agg gtc ttc ctt gag ata gtc cca cgt ctc ctc ttc Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe 340 345 350	1056
atg aag cgg ccc tcc aca gtg aaa gag aat tgc aag aag ctt att gaa Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu 355 360 365	1104
tct atg cac aaa cta acc aac tca cca agg ctt tgg tct gag acc gag Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp 370 375 380	1152
atg gag ccc aac ttc act acc tca tcc tcc ccc agc ccc cag agt aat Met Glu Pro Asn Phe Thr Thr Ser Ser Pro Ser Pro Gln Ser Asn 385 390 395 400	1200
gaa cct tca ccc aca tct tcc ttc tgt gcc cac ctt gag gag cca gcc Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala 405 410 415	1248
aaa cct atg tgc aaa tcc cct tct gga cag tac tca atg ctg cac cct Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro 420 425 430	1296
gag ccc cca cag gtg acg tgt tcc tct ccg aag ccc tcc tgc cac ccc Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro 435 440 445	1344
ctg agt gag acc cag acc aca tct atc tca aaa ggc aga tcg ctc agt Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser 450 455 460	1392

LeA34821\_SeqList

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tgt agg tcc cga agc atc cag tac tgt tac ctg cag gag gac tct tcc Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser 485 490 495	1488
cag acc aat ggc cac tct agt gcc tct cca gcg tcg cag cgc tgc cac Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His 500 505 510	1536
ctc aat gaa gag cag ccc cag cac aag ccc cac cag tgc aag tgt aag Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys 515 520 525	1584
tgc aga aag gga gag gca gct ggc aca ccg act caa gga agc aag agc Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser 530 535 540	1632
cac agc aac aaa gga gaa cac ctc gtg ctg atg tcc cca gcc ctg aag His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys 545 550 555 560	1680
ctg gcg gtg gaa ggg gtc cac tac att gca gac cac ctg cga gca gaa Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu 565 570 575	1728
gat gca gat ttc tca gtg aag gaa gac tgg aag tac gta gca atg gtc Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val 580 585 590	1776
att gac cgg atc ttt ctc tgg atg ttc atc atc gtg tgt ttg ctg ggg Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly 595 600 605	1824
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<210> 11  
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<220>  
 <223> Description of Artificial sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

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 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30  
 Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
 35 40 45  
 Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
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50 55 60  
 Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80  
 Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95  
 Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
 100 105 110  
 Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe  
 115 120 125  
 Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile  
 130 135 140  
 Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val  
 145 150 155 160  
 Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser  
 165 170 175  
 Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
 180 185 190  
 Val Asp Leu Ser Glu Phe Tyr Thr Ser Val Glu Trp Asp Ile Leu Glu  
 195 200 205  
 Val Pro Ala Val Arg Asn Glu Lys Phe Tyr Thr Cys Cys Asp Glu Pro  
 210 215 220  
 Tyr Leu Asp Ile Thr Phe Asn Phe Ile Ile Arg Arg Leu Pro Leu Phe  
 225 230 235 240  
 Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr  
 245 250 255  
 Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu  
 260 265 270  
 Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr  
 275 280 285  
 Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr  
 290 295 300  
 Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val  
 305 310 315 320  
 Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro  
 325 330 335  
 Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe  
 340 345 350  
 Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu  
 355 360 365  
 Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp  
 370 375 380  
 Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn

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385                      390                      395                      400  
 Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala  
                                  405                      410                      415  
 Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro  
                                  420                      425                      430  
 Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro  
                                  435                      440                      445  
 Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser  
                                  450                      455                      460  
 Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Gly Glu Gly Ser Ile Arg  
                                  465                      470                      475                      480  
 Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser  
                                  485                      490                      495  
 Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His  
                                  500                      505                      510  
 Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys  
                                  515                      520                      525  
 Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser  
                                  530                      535                      540  
 His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys  
                                  545                      550                      555                      560  
 Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu  
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 Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val  
                                  580                      585                      590  
 Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly  
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<210> 13  
 <211> 79  
 <212> DNA  
 <213> Artificial Sequence



LeA34821\_SeqList

<220>

<223> Description of Artificial Sequence: Primer

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<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 16

<211> 75

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<210> 17

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

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1